



1642 1600

P#15

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/646,785A

DATE: 08/07/2002

TIME: 13:03:05

Input Set : A:\soei5042us.txt

Output Set: N:\CRF4\08072002\I646785A.raw

4 <110> APPLICANT: KISHIMOTO, Tadimitsu
 5 NAGASAWA, Takashi
 6 TACHIBANA, Kazunobu
 7 CHUGAI SEIYAKU KABUSIKI KAISHA
 9 <120> TITLE OF INVENTION: Vascularization Inhibitors
 11 <130> FILE REFERENCE: 46124-5042-US
 13 <140> CURRENT APPLICATION NUMBER: US 09/646,785A
 14 <141> CURRENT FILING DATE: 2001-02-16
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP99/01448
 17 <151> PRIOR FILING DATE: 1999-03-23
 19 <150> PRIOR APPLICATION NUMBER: JP10/95448
 20 <151> PRIOR FILING DATE: 1998-03-24
 22 <160> NUMBER OF SEQ ID NOS: 12
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 352
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Mus
 29 <400> SEQUENCE: 1
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 32 Met Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg
 33 20 25 30
 34 Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr
 35 35 40 45
 36 Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
 37 50 55 60
 38 Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys
 39 65 70 75
 40 Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr
 41 80 85 90
 42 Leu Pro Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly
 43 95 100 105
 44 Asn Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu
 45 110 115 120
 46 Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr
 47 125 130 135
 48 Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu
 49 140 145 150
 50 Leu Ala Glu Lys Val Val Tyr Val Gly Val Trp Ile Pro Ala Leu
 51 155 160 165
 52 Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn Val Ser Glu Ala
 53 170 175 180
 54 Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn Asp Leu Trp

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55          185          190          195
56 Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu
57          200          205          210
58 Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser Lys
59          215          220          225
60 Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
61          230          235          240
62 Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr
63          245          250          255
64 Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile
65          260          265          270
66 Lys Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser
67          275          280          285
68 Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile
69          290          295          300
70 Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His
71          305          310          315
72 Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser
73          320          325          330
74 Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
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76 Ser Ser Ser Phe His Ser Ser
77          350

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80 <210> SEQ ID NO: 2

81 <211> LENGTH: 1588

82 <212> TYPE: DNA

83 <213> ORGANISM: Mus

85 <220> FEATURE:

86 <221> NAME/KEY: CDS

87 <222> LOCATION: (1)...(1059)

89 <400> SEQUENCE: 2

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91 atg ggc tca ggg gac tat gac tcc atg aag gaa ccc tgt ttc cgt 90
92 gaa gaa aat gct aat ttc aat aaa atc ttc ctg ccc acc atc tac 135
93 tcc atc atc ttc tta act ggc att gtg ggc aat gga ttg gtc atc 180
94 ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag 225
95 tac agg ctg cac ctg tca gtg gcc gac ctc ctc ttt gtc atc acg 270
96 ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg 315
97 aac ttc cta tgc aag gca gtc cat gtc atc tac aca gtc aac ctc 360
98 tac agc agt gtc ctc atc ctg gcc ttc atc agt ctg gac cgc tac 405
99 ctg gcc atc gtc cac gcc acc aac agt cag agg cca agg aag ctg 450
100 ttg gct gaa aag gtg gtc tat gtt ggc gtc tgg atc cct gcc ctc 495
101 ctg ctg act att ccc gac ttc atc ttt gcc aac gtc agt gag gca 540
102 gat gac aga tat atc tgt gac cgc ttc tac ccc aat gac ttg tgg 585
103 gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt atc ctg 630
104 cct ggt att gtc atc ctg tcc tgc tat tgc att atc atc tcc aag 675
105 ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acc 720
106 aca gtc atc ctc atc ctg gct ttc ttc gcc tgt tgg ctg cct tac 765
107 tac att ggg atc agc atc gac tcc ttc atc ctc ctg gaa atc atc 810

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108 aag caa ggg tgt gag ttt gag aac act gtg cac aag tgg att tcc 855
109 atc acc gag gcc cta gct ttc ttc cac tgt tgt ctg aac ccc atc 900
110 ctc tat gct ttc ctt gga gcc aaa ttt aaa acc tct gcc cag cac 945
111 gca ctc acc tct gtg agc aga ggg tcc agc ctc aag atc ctc tcc 990
112 aaa gga aag cga ggt gga cat tca tct gtt tcc act gag tct gag 1035
113 tct tca agt ttt cac tcc agc taa cacagatgta aaagactttt ttttat 1085
114 acgataaata actttttttt aagttacaca tttttcagat ataaaagact gaccaatatt 1145
115 gtacagtttt tattgtttgt tggatttttg tcttgtgttt ctttagtttt tgtgaagttt 1205
116 aattgactta tttatataaa ttttttttgt ttcattattga tgtgtgtcta ggcaggacct 1265
117 gtggccaagt tcttagttgc tgtatgtctc gtggtaggac tgtagaaaag ggaactgaac 1325
118 attccagagc gtgtagttaa tcacgtaaag cttagaatga tccccagctg tttatgcata 1385
119 gataatctct ccattcccgt ggaacgtttt tctgttctt aagacgtgat tttgctgtag 1445
120 aagatggcac ttataaccaa agcccaaagt ggtatagaaa tgctgggtttt tcagttttca 1505
121 ggagtgggtt gatttcagca cctacagtgt acagtcttgt attaagttgt taataaaagt 1565
122 acatgttaaa cttaaaaaaa aaa 1588
125 <210> SEQ ID NO: 3
126 <211> LENGTH: 359
127 <212> TYPE: PRT
128 <213> ORGANISM: Mus
130 <400> SEQUENCE: 3
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132 5 10 15
133 Glu Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys
134 20 25 30
135 Phe Arg Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr
136 35 40 45
137 Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu
138 50 55 60
139 Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr
140 65 70 75
141 Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val
142 80 85 90
143 Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp Trp Tyr
144 95 100 105
145 Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr Val
146 110 115 120
147 Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp
148 125 130 135
149 Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg
150 140 145 150
151 Lys Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro
152 155 160 165
153 Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser
154 170 175 180
155 Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg
156 185 190 195
157 Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe Gln His
158 200 205 210
159 Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys

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160		215		220		225
161	Tyr Cys Ile Ile	Ile Ser Lys Leu Ser	His Ser Lys Gly His	Gln		
162		230		235		240
163	Lys Arg Lys Ala	Leu Lys Thr Thr Val	Ile Leu Ile Leu Ala	Phe		
164		245		250		255
165	Phe Ala Cys Trp	Leu Pro Tyr Tyr Val	Gly Ile Ser Ile Asp	Ser		
166		260		265		270
167	Phe Ile Leu Leu	Gly Val Ile Lys Gln	Gly Cys Asp Phe Glu	Ser		
168		275		280		285
169	Ile Val His Lys	Trp Ile Ser Ile Thr	Glu Ala Leu Ala Phe	Phe		
170		290		295		300
171	His Cys Cys Leu	Asn Pro Ile Leu Tyr	Ala Phe Leu Gly Ala	Lys		
172		305		310		315
173	Phe Lys Ser Ser	Ala Gln His Ala Leu	Asn Ser Met Ser Arg	Gly		
174		320		325		330
175	Ser Ser Leu Lys	Ile Leu Ser Lys Gly	Lys Arg Gly Gly His	Ser		
176		335		340		345
177	Ser Val Ser Thr	Glu Ser Glu Ser Ser	Ser Phe His Ser Ser			
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181 <210> SEQ ID NO: 4

182 <211> LENGTH: 1758

183 <212> TYPE: DNA

184 <213> ORGANISM: Mus

186 <220> FEATURE:

187 <221> NAME/KEY: CDS

188 <222> LOCATION: (1)...(1080)

189 <223> OTHER INFORMATION:

191 <400> SEQUENCE: 4

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193 gaa gaa gtg ggg tct gga gac tat gac tcc aac aag gaa ccc tgc 90
194 ttc cgg gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc 135
195 atc tac ttc atc atc ttc ttg act ggc ata gtc ggc aat gga ttg 180
196 gtg atc ctg gtc atg ggt tac cag aag aag cta agg agc atg acg 225
197 gac aag tac cgg ctg cac ctg tca gtg gct gac ctc ctc ttt gtc 270
198 atc aca ctc ccc ttc tgg gca gtt gat gcc atg gct gac tgg tac 315
199 ttt ggg aaa ttt ttg tgt aag gct gtc cat atc atc tac act gtc 360
200 aac ctc tac agc agc gtt ctc atc ctg gcc ttc atc agc ctg gac 405
201 cgg tac ctc gcc att gtc cac gcc acc aac agt caa agg cca agg 450
202 aaa ctg ctg gct gaa aag gca gtc tat gtg ggc gtc tgg atc cca 495
203 gcc ctc ctc ctg act ata cct gac ttc atc ttt gcc gac gtc agc 540
204 cag ggg gac atc agt cag ggg gat gac agg tac atc tgt gac cgc 585
205 ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa ttc cag cat 630
206 ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc tcc tgt 675
207 tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac cag 720
208 aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc 765
209 ttt gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc 810
210 ttc atc ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc 855
211 att gtg cac aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc 900
212 cac tgt tgc ctg aac ccc atc ctc tat gcc ttc ctc ggg gcc aag 945

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213 ttc aaa agc tct gcc cag cat gca ctc aac tcc atg agc aga ggc 990
214 tcc agc ctc aag atc ctt tcc aaa gga aag cgg ggt gga cac tct 1035
215 tcc gtc tcc acg gag tca gaa tcc tcc agt ttt cac tcc agc taa 1080
216 cccttatgca aagacttata taatatatat atatatatga taaagaactt ttttatgtta 1140
217 cacattttcc agatataaga gactgaccag tctgtacag tttttttttt tttttaattg 1200
218 actgttgga gtttatgttc ctctagtttt tgtgagggtt gacttaattt atataaatat 1260
219 tgttttttgt ttgtttcatg tgaatgagcg tctaggcagg acctgtggcc aagttcttag 1320
220 tagctgttta tctgtgtgta ggactgtaga actgtagagg aagaaactga acattccaga 1380
221 atgtgtggta aattgaataa agctagccgt gatcctcagc tgttgctgca taatctcttc 1440
222 attccgagga gcacccccacc cccacccccca cccccacccc attcttaaat tgtttggtta 1500
223 tgctgtgtga tggtttgttt ggtttttttt tgttggtgtt gttgtttttt ttttctgtaa 1560
224 aagatggcac ttaaaaccaa agcctgaaat ggtggtagaa atgctggggt tttttttgtt 1620
225 tgtttgtttt ttcagttttc aagagtagat tgacttcagt ccctacaaat gtacagtctt 1680
226 gtattacatt gttaataaaa gtcaatgata aacttaaaaa aaaaaaaaaa aaaaaaaaaa 1740
227 aaaaaaaaaa aaaaaaaaaa 1758

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230 <210> SEQ ID NO: 5

231 <211> LENGTH: 89

232 <212> TYPE: PRT

233 <213> ORGANISM: Artificial Sequence

235 <220> FEATURE:

236 <223> OTHER INFORMATION: Ligand peptide

238 <400> SEQUENCE: 5

239 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala

240 5 10 15

241 Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys

242 20 25 30

243 Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys

244 35 40 45

245 His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val

246 50 55 60

247 Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys

248 65 70 75

249 Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys

250 80 85

253 <210> SEQ ID NO: 6

254 <211> LENGTH: 2244

255 <212> TYPE: DNA

256 <213> ORGANISM: Mus

258 <220> FEATURE:

259 <221> NAME/KEY: CDS

260 <222> LOCATION: (471)...(743)

262 <400> SEQUENCE: 6

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264 agggcccgcc ggctcgggccc agggcgcggt acctcgctcg cggggccgga gagggcgggc 120

265 ggaggcacgg ggccctggagg cgccaggcgg aggatgcggg cgacacggtg gcggcgggca 180

266 ccgcgcgacc gggcgggcggg gcgggcaggg gcgagcggag ggagggagcg gactgcggca 240

267 ggatctgtcg aggaaaaatc ttgcggcccg cgattccccg ccttttaagc gcagcctgca 300

268 ctccccccac cccacgcagg ggcgggcctt cccaacgcg ggcgcccact ggccgcccgc 360

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/646,785A

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